GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 9, 2002, 01:07:00 ; Search time 755.06 Seconds
(without alignments)
26.115 Million cell updates/sec

Title: US-09-851-670-14
Perfect score: 23
Sequence: 1 gagaacacccgctctctcgcaaa 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1026190

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_1101:*
1: /SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn/NA1982.DAT:*
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5: /SIDS2/gcgdata/geneseq/geneseqn/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn/NA1988.DAT:*
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11: /SIDS2/gcgdata/geneseq/geneseqn/NA1990.DAT:*
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19: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	14.6	63.5	50	16	AAQ88993	VEGF 2'-NH2-RNA nu
	2	14	60.9	40	14	AAQ38058	Oligonucleotide ge
	3	13.6	59.1	27	19	AAV63948	Mycobacterium tube
	4	13.6	59.1	27	20	AAX81027	Sequence of sense
	5	13.2	57.4	30	16	AAT03746	PCR primer for amp
	6	13	56.5	24	19	AAV43655	Detection probe us
	7	13	56.5	34	21	AAZ87445	S. ambofaciens spi
	8	13	56.5	34	21	AAZ90126	PCR primer for amp
c	9	13	56.5	58	18	AAV76207	Staphylococcus aur
	10	12.8	55.7	20	20	AAX33589	Oligonucleotide ta
	11	12.6	54.8	20	22	AAD11329	Human cot oncogene
c	12	12.6	54.8	27	22	AAH40207	SNP specific SNPE
c	13	12.6	54.8	27	22	AAF70982	Ligand 21A-ts. Un
c	14	12.6	54.8	35	20	AAX81412	PCR primer E1 used
	15	12.6	54.8	39	14	AAQ36898	RG678, a mutagenic
	16	12.4	53.9	20	14	AAQ41824	Baculovirus C2 com
	17	12.4	53.9	20	21	AAZ73223	Human biallelic ma
	18	12.4	53.9	26	20	AAX76977	PCR primer for his
c	19	12.4	53.9	31	22	AAI30851	Human single nucle
c	20	12.4	53.9	34	15	AAQ73469	Porcine interleuki
	21	12.4	53.9	41	15	AAQ73468	Porcine interleuki
c	22	12.4	53.9	51	22	AAH38608	Human SNP flanking
c	23	12.2	53.0	21	20	AAZ35959	Human Wnt1 PCR pri
c	24	12.2	53.0	21	22	AAS08402	Internal transcrib
c	25	12.2	53.0	24	21	AAZ95736	Barley empty donor
	26	12.2	53.0	25	21	AAZ59161	Primer #2 for huma
c	27	12.2	53.0	30	16	AAQ89021	VEGF 2'-NH2-RNA nu
	28	12.2	53.0	40	17	AAT69463	Plasmid p182SfiI c
c	29	12.2	53.0	40	17	AAT69469	Plasmid p182SfiI c
	30	12.2	53.0	40	20	AAX88887	Circular plasmid e
c	31	12.2	53.0	40	20	AAX88893	Circular plasmid e
	32	12.2	53.0	43	20	AAX18868	Maize SSR oligonuc
	33	12.2	53.0	43	20	AAX18871	Maize SSR oligonuc
	34	12.2	53.0	43	20	AAX18874	Maize SSR oligonuc
	35	12.2	53.0	44	21	AAA75400	Fragment derived f
	36	12.2	53.0	50	20	AAX52072	Synthetic plasmid
	37	12	52.2	20	15	AAQ74652	Aspergillus aculea
	38	12	52.2	25	19	AAV38473	Human CC chemokine
c	39	12	52.2	26	16	AAQ98435	Truncated 2'-NH2 b
c	40	12	52.2	26	16	AAQ98439	Control oligo, deo
c	41	12	52.2	26	16	AAQ98438	Truncated bFGF RNA
c	42	12	52.2	26	18	AAT65452	Basic fibroblast g
c	43	12	52.2	26	22	AAF70724	Oligonucleotide #1
c	44	12	52.2	26	22	AAF70983	Control ligand deo
	45	12	52.2	27	20	AAX81123	PCR primer for clo

ALIGNMENTS

RESULT 1
AAQ88993/c
ID AAQ88993 standard; RNA; 50 BP.
XX
AC AAQ88993;
XX
DT 28-SEP-1995 (first entry)
XX
DE VEGF 2'-NH2-RNA nucleic acid ligand family 2, oligo 23B.
XX
KW Nucleic acid; ligand; thrombin; elastase; theophylline; caffeine;
KW pharmaceutical; diagnosis; vascular endothelial growth factor;
KW gene therapy; RNA; DNA; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /note= "2'-NH2-Cytosine"
XX
PN WO9507364-A.
XX
PD 16-MAR-1995.
XX
PF 08-SEP-1994; 94WO-US10306.
XX
PR 08-SEP-1993; 93US-0117991.
PR 07-OCT-1993; 93US-0134028.
PR 22-FEB-1994; 94US-0199507.
PR 25-APR-1994; 94US-0233012.
PR 28-APR-1994; 94US-0234997.
XX
PA (NEXA-) NEXAGEN INC.

```
XX
PI   Biesecker G,  Gold L,  Janjic N,  Jayasena S,  Jenison RD;
PI   Kirschenheuter GP,  Pieken W,  Polisky B,  Smith D,  Tasset D;
XX
DR   WPI; 1995-123436/16.
XX
PT   Identifying nucleic acid ligands for target molecules - by
PT   partitioning increased affinity nucleic acids from a candidate
PT   mixt. and amplifying
XX
PS   Claim 37; Fig 34; 251pp; English.
XX
CC   The sequences given in AAQ88993-98 represent nucleic acid ligands to
CC   vascular endothelial growth factor (VEGF).  These ligands all
CC   contain the consensus sequence given in AAQ88999.  These ligands were
CC   identified using the method of the invention.  The method comprises
CC   contacting a candidate mixture with the target molecule (i.e. VEGF)
CC   where the nucleic acids which have an increased affinity to the target
CC   relative to the candidate mixture can be partitioned from the remainder
CC   of the candidate mixture.  The increased affinity nucleic acids are
CC   partitioned from the remainder of the candidate mixture and the isolated
CC   nucleic acids are amplified to yield a ligand-enriched mixture of
CC   nucleic acids, in which the nucleic acid ligands can be identified.
CC   The isolated ligands may be used as pharmaceuticals, diagnostic agents
CC   and in gene therapy.  The ligands may be RNA or DNA molecules.
XX
SQ   Sequence 50 BP; 11 A; 12 C; 19 G; 8 U; 0 other;


  Query Match             63.5%;  Score 14.6;  DB 16;  Length 50;
  Best Local Similarity   81.0%;  Pred. No. 3.4e+02;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2 agaacacccgctctctcgcaa 22
           ||||| |||||||| | | ||
Db      28 AGAACCCCCGCTCTGTTGTAA 8


RESULT   2
AAQ38058
ID   AAQ38058 standard; DNA; 40 BP.
XX
AC   AAQ38058;
XX
DT   07-JUL-1993  (first entry)
XX
DE   Oligonucleotide gel15, for prodn. of synthetic gelonin gene.
XX
KW   Seed; toxin; plant; cloning; ribosomal; protein synthesis; ss;
KW   Gelonium multiflorum.
XX
OS   Synthetic.
XX
PN   WO9305168-A.
XX
PD   18-MAR-1993.
XX
PF   21-AUG-1992;   92WO-US07066.
XX
PR   06-SEP-1991;   91US-0755949.
XX
PA   (RERE-) RES DEV FOUND.
XX
PI   Beattie KL,  Rosenblum MG;
XX
DR   WPI; 1993-100990/12.
XX
PT   Synthetic DNA encoding gelonin plant toxin - provides nucleotide
PT   sequence for synthetic gene for prodn. and cloning
XX
PS   Example 4; Fig 5; 45pp; English.
XX
CC   The synthetic gelonin gene based on the sequence of Gelonium
CC   multiflorum gelonin was prepd. by synthesising a number of
CC   oligonucleotides corresp. to fragments of the gelonin gene and
CC   annealing and ligating to assemble the intact gene.  The
CC   oligonucleotides were designed to contain a codon triplet for each
CC   amino acid in the corresp. gelonin fragment.  Gelonin is a ribosomal-
CC   inactivating plant toxin which inhibits protein synthesis.  The
CC   synthetic form of gelonin provides a plentiful, reproducible source
CC   of gelonin which may be modified.
CC   See also AAQ38041-82.
XX
SQ   Sequence 40 BP; 12 A; 14 C; 7 G; 7 T; 0 other;


  Query Match             60.9%;  Score 14;  DB 14;  Length 40;
  Best Local Similarity   77.3%;  Pred. No. 6.5e+02;
  Matches   17;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2 agaacacccgctctctcgcaaa 23
           | ||||||  |||||| | |||
Db      17 acaacaccatctctctggaaaa 38


RESULT   3
AAV63948
ID   AAV63948 standard; DNA; 27 BP.
XX
AC   AAV63948;
XX
DT   21-JAN-1999  (first entry)
XX
DE   Mycobacterium tuberculosis sense oligonucleotide pvR3.
XX
KW   Mycobacterium tuberculosis; antigen; vaccine; immunological;
KW   immunogen; infection; primer; ss.
XX
OS   Synthetic.
OS   Mycobacterium tuberculosis.
XX
PN   WO9844119-A1.
XX
PD   08-OCT-1998.
XX
PF   01-APR-1998;   98WO-DK00132.
XX
PR   05-JAN-1998;   98US-0070488.
PR   02-APR-1997;   97DK-0000376.
PR   18-APR-1997;   97US-0044624.
PR   10-NOV-1997;   97DK-0001277.
XX
PA   (STAT-) STATENS SERUM INST.
XX
PI   Andersen P,  Florio W,  Nielsen R,  Oettinger T,  Rasmussen PB;
PI   Rosenkrands I,  Weldingh K;
XX
DR   WPI; 1998-542705/46.
XX
PT   New isolated mycobacteria polypeptides and nucleic acids - used for
PT   developing products for the diagnosis of or vaccination against
PT   mycobacterial infections, particularly tuberculosis
XX
PS   Example 2; Page 52; 163pp; English.
XX
CC   The present sequence represents an oligonucleotide used in an example
CC   from the present invention. Products from the present invention, which
CC   describes protein fragments and nucleic acid fragments derived from
CC   M. tuberculosis, can be used in the detection of and prevention of
CC   mycobacterial infections. In particular, the proteins and nucleic acids
CC   can be used for the diagnosis of or vaccination against tuberculosis
CC   caused by M. tuberculosis, M. africanum or M. bovis.
XX
SQ   Sequence 27 BP; 8 A; 8 C; 7 G; 4 T; 0 other;
```

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  Query Match             59.1%;  Score 13.6;  DB 19;  Length 27;
  Best Local Similarity   80.0%;  Pred. No. 9.7e+02;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      4 aacacccgctctctcgcaaa 23
          ||||||||   | |||||||
Db      3 aacacccgggatgtcgcaaa 22


RESULT   4
AAX81027
ID   AAX81027 standard; DNA; 27 BP.
XX
AC   AAX81027;
XX
DT   06-SEP-1999  (first entry)
XX
DE   Sequence of sense oligo pvR3.
XX
KW   Immunogenic; Mycobacterium tuberculosis; immune response; infection;
KW   tuberculosis; fusion polypeptide; T-cell epitope; ESAT-6; MPT59; TB;
KW   pharmaceutical; vaccination; M. africanum; M. bovis; CFP7A; CFP30A;
KW   CFP7B; CFP19; CFP27; CFP30A; RD1-ORF; CFP10A; CFP16; CFP19; CFP23;
KW   CFP25A; CFP30B; CFP7B; PCR primer; ss.
XX
OS   Synthetic.
OS   Mycobacterium tuberculosis.
XX
PN   WO9924577-A1.
XX
PD   20-MAY-1999.
XX
PF   08-OCT-1998;   98WO-DK00438.
XX
PR   01-APR-1998;   98WO-DK00132.
PR   10-NOV-1997;   97DK-0001277.
PR   05-JAN-1998;   98US-0070488.
XX
PA   (STAT-) STATENS SERUM INST.
XX
PI   Andersen P,  Skjot R;
XX
DR   WPI; 1999-347282/29.
XX
PT   New immunogenic fragment of Mycobacterium tuberculosis
XX
PS   Example 1; Page 45; 265pp; English.
XX
CC   The invention describes a substantially pure immunogenic polypeptide
CC   fragment (I) from Mycobacterium tuberculosis that is able to evoke a
CC   protective immune response against infections by mycobacteria belonging
CC   to the tuberculosis complex. The invention provides a (1) fusion
CC   polypeptide comprising at least one polypeptide fragment (I) and at least
CC   one fusion partner; (2) a fusion polypeptide fragment comprising a T-cell
CC   epitope from M. tuberculosis protein ESAT-6, or MPT59 and a second
CC   different amino acid sequence from M. tuberculosis, and/or including a
CC   sequence which protects the first amino acid sequence from in vivo
CC   degradation or post-translational processing; (3) a nucleic acid fragment
CC   that encodes the above polypeptides. The polypeptides and nucleic acid
CC   are useful as pharmaceuticals, for diagnosis of and as antigens for
CC   vaccination against TB caused by Mycobacterium tuberculosis, africanum or
CC   bovis. The polypeptides are also useful for diagnosing ongoing or
CC   previous sensitization in an animal with bacteria belonging to the
CC   tuberculosis complex. The invention also describes the use of CFP7A or
CC   CFP30A or a T-cell epitope of for the induction of a strong immune
CC   response in a mammal; use of CFP7B, CFP19 or MPT59-ESAT6 or a T-cell
CC   epitope of for diagnosis of TB in a mammal by performing a DTH type skin
CC   test; use of CFP27, CFP30A, RD1-ORF2, RD1-ORF3, RDI-ORF5, MPT59-ESAT6,
CC   ESAT6-MPT59, CFP10A, CFP16, CFP19, CFP23, CFP25A, CFP30B, CFP7B or a T-
CC   cell epitope of for the preparation of an immunological composition; and
CC   for the preparation of a subunit vaccine.
XX
SQ   Sequence 27 BP; 8 A; 8 C; 7 G; 4 T; 0 other;

  Query Match             59.1%;  Score 13.6;  DB 20;  Length 27;
  Best Local Similarity   80.0%;  Pred. No. 9.7e+02;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      4 aacacccgctctctcgcaaa 23
          ||||||||   | |||||||
Db      3 aacacccgggatgtcgcaaa 22


RESULT   5
AAT03746
ID   AAT03746 standard; cDNA; 30 BP.
XX
AC   AAT03746;
XX
DT   28-MAR-1996  (first entry)
XX
DE   PCR primer for amplifying gax gene.
XX
KW   Gax; smooth muscle cell; proliferation; inhibition; gene therapy;
KW   atheromatous plaque; balloon angioplasty; artery; ss.
XX
OS   Synthetic.
XX
PN   WO9523161-A1.
XX
PD   31-AUG-1995.
XX
PF   22-FEB-1995;   95WO-US01882.
XX
PR   24-FEB-1994;   94US-0203532.
XX
PA   (UYCA-) UNIV CASE WESTERN RESERVE.
XX
PI   Gorski DH,  Walsh K;
XX
DR   WPI; 1995-311500/40.
XX
PT   Rat and human growth arresting homeo-box gene - inhibits vascular
PT   smooth muscle cell growth, useful in treatment of blood vessel
PT   diseases
XX
PS   Disclosure; Page 16; 48pp; English.
XX
CC   The Gax protein (AAR82096 (rat) or AAR82097 (human)) can be used for
CC   inhibiting the proliferation of eukaryotic cells, esp. vascular smooth
CC   muscle cell proliferation by gene therapy.  The gax gene (AAT03744
CC   (rat) or AAT03745 (human)) or fragment of it may be administered to
CC   the interior wall during balloon angioplasty to inhibit the
CC   proliferation of vascular smooth muscle cells and reduce the chances
CC   of the formation of atheromatous plaques and internal arterial
CC   thickening. Two primers (AAT03746, AAT03747) were used to amplify the
CC   coding region of the gax cDNA spanning nucleotides 200-1108 for its
CC   subcloning into an expression vector and the production of a
CC   Glutathione-S-transferase-Gax fusion protein.
XX
SQ   Sequence 30 BP; 4 A; 13 C; 8 G; 5 T; 0 other;


  Query Match             57.4%;  Score 13.2;  DB 16;  Length 30;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      3 gaacacccgctctctcgc 20
          |||||||| |||| | ||
Db     13 gaacacccccctctttggc 30


RESULT   6
AAV43655
ID   AAV43655 standard; DNA; 24 BP.
```

XX
AC AAV43655;
XX
DT 28-SEP-1998 (first entry)
XX
DE Detection probe used in target-triggered amplification.
XX
KW Promoter sequestered oligonucleoside; CPS; RNA polymerase promoter;
KW target-triggered amplification; probe; ss.
XX
OS Synthetic.
OS Bacteriophage t7.
XX
PN EP851033-A1.
XX
PD 01-JUL-1998.
XX
PF 23-DEC-1997; 97EP-0310550.
XX
PR 30-DEC-1996; 96US-0770941.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Becker MM, Myers KK, Stull PD;
XX
DR WPI; 1998-335379/30.
XX
PT Promoter-sequestered oligonucleoside used in trigger amplification
PT of nucleic acid - comprises complementary first and second nucleic
PT acid sequences and single-stranded loop containing RNA polymerase
PT promoter
XX
PS Example 1; Page 13; 39pp; English.
XX
CC The present sequence represents a detection probe used to exemplify
CC the method of invention. The invention provides promoter-sequestered
CC oligonucleoside which has a stem comprising first and second nucleic
CC acid sequences, which are substantially complementary to each other and
CC a single-stranded loop region located between the first and second
CC sequence, where all, or a portion, of an RNA polymerase promoter
CC sequence is located within the loop region. The promoter-sequestered
CC oligonucleoside is used in trigger amplification of a nucleic acid
CC sequence in the presence of a target sequence by combining with a sample
CC comprising the target sequence, under amplifying conditions, forming a
CC functional double-stranded promoter region and producing multiple copies
CC of nucleic acid using the target sequence or the target-complementary
CC sequence as a template under RNA polymerase mediated amplification
CC conditions. It can also detect the nucleic acid sequence, by combining
CC it and the sample, under amplifying conditions, forming a functional
CC double-stranded promoter region if the target sequence is present in
CC the sample, producing RNA transcripts under RNA polymerase mediated
CC amplification conditions using the functional promoter and detecting
CC whether RNA transcripts are produced.
XX
SQ Sequence 24 BP; 8 A; 9 C; 3 G; 4 T; 0 other;

Query Match 56.5%; Score 13; DB 19; Length 24;
Best Local Similarity 76.2%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 agaacacccgctctctcgcaa 22
|||||||| || || || ||
Db 2 agaacaccacctttcgcgaaa 22

RESULT 7
AAZ87445
ID AAZ87445 standard; DNA; 34 BP.
XX
AC AAZ87445;
XX
DT 22-MAY-2000 (first entry)
XX
DE S. ambofaciens spiramycin PKS loading domain PCR primer #9.
XX
KW Polyketide; macrolide; biosynthesis; polyketide synthase; PKS;
KW multienzyme complex; loading module; ketosynthase domain; KS; CLF domain;
KW decarboxylation; acyl carrier protein domain; ACP; anthelminthic;
KW insecticide; immunosuppressant; antifungal; antibacterial; spiramycin;
KW hybrid PKS; PCR primer; ss.
XX
OS Streptomyces ambofaciens.
XX
PN WO200000618-A2.
XX
PD 06-JAN-2000.
XX
PF 29-JUN-1999; 99WO-GB02044.
XX
PR 29-JUN-1998; 98GB-0014006.
XX
PA (BIOT-) BIOTICA TECHNOLOGY LTD.
XX
PI Leadlay PF, Staunton J, Cortes J, McArthur HAI;
XX
DR WPI; 2000-170919/15.
XX
PT Novel methods for preparing new variant polyketides, for use as
PT anthelminthics, insecticides, immunosuppressants, antifungals or
PT antibacterials -
XX
PS Example 16; Page 53; 97pp; English.
XX
CC The invention relates to a novel system for producing polyketides
CC particularly 12-, 14- and 16-membered ring macrolides from a desired
CC starter unit. The biosynthesis of polyketides is initiated by a group
CC of chain-forming enzymes known as polyketide synthases (PKSs) which are
CC multienzyme complexes consisting of a set, or module, of enzymes
CC which catalyse polyketide chain extension. The system of the
CC invention comprises inserting loading modules into PKSs that do not
CC normally possess them, thereby controlling the starter units used. The
CC loading module may be adapted to load an optionally substituted malonyl
CC residue, which it then decarboxylates to provide an optionally
CC substituted acetyl residue for transfer to a chain extension module. The
CC loading module comprises a KS (ketosynthase)-type domain which effects
CC decarboxylation, and an acyl carrier protein domain (ACP). The KS-type
CC domain is preferably a Ksq domain, which possesses a glutamine rather
CC than a cysteine in the active site. Alternatively a CLF-type domain,
CC which also contains a glutamine at this site, may provide the
CC decarboxylating functionality. The methods of the invention are used to
CC produce polyketides, particularly 12-, 14- and 16-membered ring
CC macrolides. The system is used to produce macrolides with preferred
CC (acetate or propionate) starter units, or with unusual starter units,
CC which minimises the formation of by-products containing a different
CC starter unit. The polyketides produced have use as potential
CC anthelminthics, insecticides, immunosuppressants, antifungals or
CC antibacterials. The present invention provides a system for producing
CC polyketides which minimises the formation of by-products containing an
CC undesired or different starter units, and also allows the incorporation
CC of unusual starter units. The system allows the identification of
CC polyketides which may have enhanced properties or possess novel
CC bioactivity. Sequences AAZ87437-Z87456 represent PCR primers used in
CC exemplifications of the present invention to amplify DNA encoding
CC PKS functional domains of a variety of actinomycetes. The amplified
CC DNA was then used in the construction of genes encoding hybrid
CC polyketide synthases.
XX
SQ Sequence 34 BP; 7 A; 10 C; 8 G; 9 T; 0 other;

Query Match 56.5%; Score 13; DB 21; Length 34;
Best Local Similarity 76.2%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 gagaacacccgctctctcgca 21

```
          |||||| | || | || ||||
Db     12 gagaactcgcgatttcccgca 32


RESULT   8
AAZ90126
ID   AAZ90126 standard; DNA; 34 BP.
XX
AC   AAZ90126;
XX
DT   19-MAY-2000  (first entry)
XX
DE   PCR primer for amplifying a spiramycin producing PKS gene fragment.
XX
KW   14-member macrolide; spiramycin-producing loading module; antibiotic;
KW   polyketide synthase; PKS; PCR primer; ss.
XX
OS   Streptomyces ambofaciens.
XX
PN   WO200000500-A2.
XX
PD   06-JAN-2000.
XX
PF   29-JUN-1999;   99WO-GB02042.
XX
PR   29-JUN-1998;   98GB-0014006.
XX
PA   (BIOT-) BIOTICA TECHNOLOGY LTD.
PA   (PFIZ ) PFIZER INC.
XX
PI   Leadlay PF,  Staunton J,  Cortes J,  McArthur HAI;
XX
DR   WPI; 2000-170901/15.
XX
PT   New 14-member macrolides incorporating acetate starter unit, used as
PT   antibiotics -
XX
PS   Example 8; Page 38; 78pp; English.
XX
CC   This sequence represents a PCR primer used to amplify the
CC   spiramycin-producing loading module from the Streptomyces ambofaciens
CC   polyketide synthase (PKS) genes. PKS is used in a system for the
CC   production of the macrolides of the invention. The macrolides are
CC   14-member macrolides that incorporate an acetate starter unit so that it
CC   has a 13-methyl substituent, provided that it is not norerythromycin C,
CC   6-deoxy-15-norerythromycin B or 6-deoxy-15-norerythromycin D. The new
CC   14-member macrolides may be used as antibiotics. The macrolides are
CC   produced by a process which minimizes the formation of by-products
CC   containing different starter units. 13-Methyl erythromycins can be
CC   produced at good expression levels and in substantial absence of
CC   erythromycins with different starter units. Chemical modifications
CC   previously only possible with 'natural' erythromycins can be performed.
XX
SQ   Sequence 34 BP; 7 A; 10 C; 8 G; 9 T; 0 other;


  Query Match             56.5%;  Score 13;  DB 21;  Length 34;
  Best Local Similarity   76.2%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      1 gagaacacccgctctctcgca 21
          |||||| | || | || ||||
Db     12 gagaactcgcgatttcccgca 32


RESULT   9
AAV76207/c
ID   AAV76207 standard; DNA; 58 BP.
XX
AC   AAV76207;
XX
DT   16-MAR-1999  (first entry)
XX
DE   Staphylococcus aureus contig SEQ ID #1896.
XX
KW   Computer readable medium; vaccine; S.aureus infection; immunodetection;
KW   cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
KW   skin infection; surgical wound infection; scalded skin syndrome;
KW   toxic shock syndrome; ds.
XX
OS   Staphylococcus aureus.
XX
PN   EP786519-A2.
XX
PD   30-JUL-1997.
XX
PF   07-JAN-1997;   97EP-0100117.
XX
PR   05-JAN-1996;   96US-0009861.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Barash SC,  Choi GH,  Dillon PJ,  Fannon MR,  Kunsch CA;
PI   Rosen CA;
XX
DR   WPI; 1997-374922/35.
XX
PT   Polynucleotide(s) and proteins derived from Staphylococcus aureus -
PT   stored on computer readable medium and used in the production of
PT   anti-S.aureus vaccines
XX
PS   Claim 1; Page 2089; 3271pp; English.
XX
CC   This sequence represents one of 5191 Staphylococcus aureus DNA sequences
CC   of the invention. The DNA sequences are recorded on a computer readable
CC   medium, preferably selected from a floppy or hard disk, random access
CC   memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
CC   the S.aureus DNA sequences allows putative functions to be assigned so
CC   that protein-encoding or regulatory regions of commercial, therapeutic or
CC   industrial importance can be obtained. Specifically, sequences which are
CC   likely to encode antigens have been identified and these polypeptides can
CC   be used in a vaccine composition against S.aureus infection. The
CC   polypeptides can also be used in a kit for the immunodetection of
CC   S.aureus in a sample. S.aureus is implicated in numerous human diseases,
CC   including cellulitis, eyelid infections, food poisoning, osteomyelitis,
CC   skin and surgical wound infections, scalded skin syndrome, toxic shock
CC   syndrome, etc. Organisms transformed with the DNA sequences can be used
CC   for recombinant production of the polypeptides. The new DNA sequences
CC   (and their fragments) are useful as primers or probes for isolating
CC   homologues of any of the S.aureus DNA sequences contained on the
CC   computer readable medium.
XX
SQ   Sequence 58 BP; 6 A; 14 C; 19 G; 19 T; 0 other;


  Query Match             56.5%;  Score 13;  DB 18;  Length 58;
  Best Local Similarity   76.2%;  Pred. No. 2.1e+03;
  Matches   16;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      3 gaacacccgctctctcgcaaa 23
          |||||||| | ||   |||||
Db     33 GAACACCCACGCTGCGGCAAA 13


RESULT  10
AAX33589
ID   AAX33589 standard; DNA; 20 BP.
XX
AC   AAX33589;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Oligonucleotide tag 20-mer #5.
XX
KW   Labelling; tag; molecular species; identification; property;
KW   characteristic; hybridisation; amplification; ss.
```

XX
OS Synthetic.
XX
PN WO9918240-A2.
XX
PD 15-APR-1999.
XX
PF 05-OCT-1998; 98WO-US20874.
XX
PR 06-OCT-1997; 97US-0944410.
XX
PA (STRA-) STRATAGENE.
XX
PI Sorge JA;
XX
DR WPI; 1999-264040/22.
XX
PT Uniquely tagged molecules identifiable by a unique property or
PT characteristic
XX
PS Disclosure; Page 45; 138pp; English.
XX
CC The present invention describes a composition comprising a mixture of
CC different species of molecules where each species is linked to a tag
CC that is unique to that species and that encodes at least two variable
CC positions on that species, where the tags can be identified without the
CC need for first isolating each of the tags prior to identification. Liquid
CC phase hybridisation system may be used for simultaneous identification
CC of a large subset of targets out of a very large collection of similar
CC of dissimilar molecular species. It may also be used to create tagged
CC molecules that identify any collection of molecular species, e.g.
CC peptides, antibodies, nucleic acids. Method bar codes collections or
CC probes or analytes for use in a liquid phase hybridisation method. Tagged
CC probes able to detect small changes or mutations in the target specimen.
CC Use of molecular tags overcomes difficulties of prior art methods, e.g.
CC the concentration of the probe would not be limited by the solid support,
CC both the target nucleic acids and the probes can diffuse toward each
CC other, and signal amplification through cycling reactions could occur.
CC Sequencing DNA with tags in combination with DNA amplification techniques
CC means that there is no need for traditional sequencing methods or
CC attaching to a solid phase, either the materials to be analysed or the
CC tags. The present sequence represents an oligonucleotide tag from the
CC present invention.
XX
SQ Sequence 20 BP; 3 A; 10 C; 3 G; 4 T; 0 other;

Query Match 55.7%; Score 12.8; DB 20; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       5 acacccgctctctcgc 20
           |||| ||||| |||||
Db       4 acactcgctcgctcgc 19
```

RESULT 11
AAD11329
ID AAD11329 standard; DNA; 20 BP.
XX
AC AAD11329;
XX
DT 24-SEP-2001 (first entry)
XX
DE Human cot oncogene antisense oligonucleotide, ISIS 116370.
XX
KW Human; cot oncogene; antisense therapy; inflammation; cancer; antisense;
KW immune system disorder; prophylaxis; cytostatic; immunomodulator;
KW Tpl-2; est; phosphorothioate backbone; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX

FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 5
FT /*tag= c
FT /mod_base= m5c
FT modified_base 9
FT /*tag= d
FT /mod_base= m5c
FT modified_base 10
FT /*tag= e
FT /mod_base= m5c
FT modified_base 11
FT /*tag= f
FT /mod_base= m5c
FT modified_base 13
FT /*tag= g
FT /mod_base= m5c
FT modified_base 14
FT /*tag= h
FT /mod_base= m5c
FT modified_base 15
FT /*tag= i
FT /mod_base= m5c
FT modified_base 16..20
FT /*tag= j
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 17
FT /*tag= k
FT /mod_base= m5c
FT modified_base 19
FT /*tag= l
FT /mod_base= m5c
FT modified_base 20
FT /*tag= m
FT /mod_base= m5c
XX
PN US6265216-B1.
XX
PD 24-JUL-2001.
XX
PF 20-JAN-2000; 2000US-0489868.
XX
PR 20-JAN-2000; 2000US-0489868.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Wyatt J;
XX
DR WPI; 2001-463936/50.
XX
PT New antisense oligonucleotides for modulating cot oncogene expression,
PT particularly useful for diagnosing or treating diseases associated with
PT expression of cot oncogene, such as inflammation, cancer or immune
PT system disorders -
XX
PS Example 15; Column 41; 39pp; English.
XX
CC The invention relates to antisense oligonucleotides, compositions
CC and methods for modulating cot oncogene expression. The cot oncogene
CC is also known as Tpl-2 and est. The compositions comprise antisense
CC compounds, particularly antisense oligonucleotides, targetted to
CC nucleic acids encoding cot oncogene. The antisense oligonucleotides
CC are useful for modulating the expression of cot oncogene and for
CC treating diseases associated with expression of cot oncogene, e.g.
CC inflammation, cancer or disorders of the immune system. The antisense

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CC   oligonucleotides are also useful for diagnosis or prophylaxis or as
CC   research reagents and kits. The present sequence is human cot oncogene
CC   antisense oligonucleotide, ISIS 116370. This sequence was targetted
CC   towards the coding region of human cot oncogene.
XX
SQ   Sequence 20 BP; 5 A; 10 C; 3 G; 2 T; 0 other;


  Query Match             54.8%;  Score 12.6;  DB 22;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 2.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      2 agaacacccgctctctcgc 20
          ||||||  | ||| |||||
Db      1 agaacagaccctccctcgc 19


RESULT  12
AAH40207/c
ID   AAH40207 standard; DNA; 27 BP.
XX
AC   AAH40207;
XX
DT   14-AUG-2001  (first entry)
XX
DE   SNP specific SNPE primer SEQ ID 3003.
XX
KW   Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW   SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW   Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW   polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW   acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW   inflammation; forensic investigation; paternity analysis; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200129262-A2.
XX
PD   26-APR-2001.
XX
PF   13-OCT-2000; 2000WO-US28436.
XX
PR   15-OCT-1999;   99US-0160096.
XX
PA   (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI   Picoult-Newburg L,  Pohl M;
XX
DR   WPI; 2001-290930/30.
XX
PT   New genotyping oligonucleotide, useful for detecting the presence,
PT   absence or identity of single polynucleotide polymorphism in a nucleic
PT   acid sample  -
XX
PS   Claim 1; Page 65; 83pp; English.
XX
CC   Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC   primer extension (SNPE) primers, and the sequences of regions flanking
CC   sites of single nucleotide polymorphisms SNPs. The present invention
CC   includes kits for determining the presence or absence of a SNP, using the
CC   oligonucleotides of the invention. The PCR primers are used to amplify a
CC   SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC   The oligonucleotides are useful for genotyping a nucleic acid sample by
CC   performing a single-nucleotide primer extension reaction. The
CC   oligonucleotides are useful for determining the presence, absence or
CC   identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC   assess by association analysis the genotype of an individual or group of
CC   individuals, having a pathological phenotypic trait suspected of being
CC   caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC   agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC   dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC   osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC   traits also include symptoms of or susceptibility to multifactorial
CC   disease of which a component is or may be genetic such as autoimmune
CC   diseases, including, rheumatoid arthritis, multiple sclerosis,
CC   inflammation, cancer, nervous system diseases and infection by pathogenic
CC   microorganism. The method is also useful in forensic investigations and
CC   paternity analysis. The present sequence represents a single nucleotide
CC   primer extension (SNPE) primer specific for a human SNP containing DNA
CC   sequence.
XX
SQ   Sequence 27 BP; 4 A; 5 C; 11 G; 6 T; 1 other;


  Query Match             54.8%;  Score 12.6;  DB 22;  Length 27;
  Best Local Similarity   75.0%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      2 agaacacccgctctctcgca 21
          | | || ||||  |||||||
Db     23 ACANCAACCGCCATCTCGCA 4


RESULT  13
AAF70982/c
ID   AAF70982 standard; DNA; 27 BP.
XX
AC   AAF70982;
XX
DT   20-APR-2001  (first entry)
XX
DE   Ligand 21A-ts.
XX
KW   Ligand; basic fibroblast growth factor; bFGF; gene therapy; vascular;
KW   atherosclerosis; angioplasty; stability; ss.
XX
OS   Unidentified.
XX
PN   US6177557-B1.
XX
PD   23-JAN-2001.
XX
PF   05-AUG-1996;   96US-0687421.
XX
PR   11-JUN-1990;   90US-0536428.
PR   10-JUN-1991;   91US-0714131.
PR   06-NOV-1992;   92US-0973333.
PR   10-FEB-1994;   94US-0195005.
PR   28-MAR-1994;   94US-0219012.
XX
PA   (NEXS-) NEXSTAR PHARM INC.
XX
PI   Janjic N,  Gold L,  Tasset D;
XX
DR   WPI; 2001-158583/16.
XX
PT   Novel nucleic acid ligands to basic fibroblast growth factor that are
PT   useful as inhibitors of basic fibroblast growth factors and 2'-amino
PT   modified RNA ligands, exhibit increased in vivo stability  -
XX
PS   Claim 1; Column 27; 153pp; English.
XX
CC   The present invention relates to a purified and isolated non-naturally
CC   occurring DNA ligands to basic fibroblast growth factor (bFGF).
CC   The ligands are useful as part of gene therapy treatments and
CC   for diagnosing pathogenesis of vascular diseases including
CC   initiation and progression of atherosclerosis, acute coronary
CC   syndromes, vein graft disease and restenosis following coronary
CC   angioplasty. The ligands have improved stability in vivo.
XX
SQ   Sequence 27 BP; 4 A; 3 C; 13 G; 6 U; 1 other;


  Query Match             54.8%;  Score 12.6;  DB 22;  Length 27;
  Best Local Similarity   69.6%;  Pred. No. 3e+03;
  Matches   16;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;
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```
Qy      1 gagaacacccgctctctcgcaaa 23
          |: | |||||||| |||  || |
Db     27 GHAACCACCCGCTGTCTTCCACA 5
```

RESULT 14
AAX81412/c
ID AAX81412 standard; DNA; 35 BP.
XX
AC AAX81412;
XX
DT 25-AUG-1999 (first entry)
XX
DE PCR primer E1 used to amplify a human airway trypsin protease intron.
XX
KW Human airway trypsin protease; intron; disease predisposition;
KW polymorphism; respiratory disease; chronic obstructive pulmonary disease;
KW sinobronchial syndrome; pulmonary emphysema; diffuse bronchiolitis;
KW bronchiectasis; abnormal muco-cilia bio-defence system; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9931271-A1.
XX
PD 24-JUN-1999.
XX
PF 16-DEC-1998; 98WO-JP05689.
XX
PR 16-DEC-1997; 97JP-0346494.
XX
PA (TEIJ) TEIJIN LTD.
XX
PI Eguchi H, Masuda K, Yamaoka K, Yasuoka S;
XX
DR WPI; 1999-395192/33.
XX
PT Human airway trypsin protease gene polymorphism-based prediction of
PT predisposition of individuals to specific diseases (claimed),
PT therapeutic effect or prognosis following treatments
XX
PS Claim 5; Page 41; 55pp; Japanese.
XX
CC PCR primers AAX81412-13 were used to amplify an intron of human airway
CC trypsin protease. The specification describes a method for prediction of
CC the predisposition of individuals to specific diseases, or therapeutic
CC effect on the patients or the prognosis following the treatments. The
CC method is based on the analysis of human airway trypsin protease gene
CC polymorphism. The method is used for diagnosis and therapy. The ability
CC to forecast relapse after treatment can be achieved by this method, as
CC well as the determination of predisposition of individuals to specific
CC diseases, e.g. respiratory diseases, including chronic obstructive
CC pulmonary disease, sinobronchial syndrome, pulmonary emphysema, diffuse
CC bronchiolitis and bronchiectasis. The methods can also be used for
CC diagnosis of abnormal muco-cilia bio-defence system.
XX
SQ Sequence 35 BP; 8 A; 2 C; 16 G; 9 T; 0 other;

```
  Query Match             54.8%;  Score 12.6;  DB 20;  Length 35;
  Best Local Similarity   78.9%;  Pred. No. 3.1e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      4 aacacccgctctctcgcaa 22
          |||| |||||||| | | |
Db     35 AACATCCGCTCTCACACCA 17
```

RESULT 15
AAQ36898
ID AAQ36898 standard; DNA; 39 BP.
XX
AC AAQ36898;
XX
DT 15-JUN-1993 (first entry)
XX
DE RG678, a mutagenic PCR primer.
XX
KW FPV; fowlpox virus; infectious bursal disease virus; IBDV; vaccine;
KW Fargher; STC; TROVAC; VP2; ss.
XX
PN WO9303145-A.
XX
PD 18-FEB-1993.
XX
PF 22-JUL-1992; 92WO-US06100.
XX
PR 26-JUL-1991; 91US-0736254.
PR 21-JUL-1992; 92US-0918311.
XX
PA (VIRO-) VIROGENETICS CORP.
XX
PI Gettig R, Paoletti E, Taylor J;
XX
DR WPI; 1993-076502/09.
XX
PT Recombinant pox-virus contg. infectious bursal disease virus DNA
PT - used to produce vaccines for providing protective immunity
PT against IBDV infections, partic. in poultry
XX
PS Example 10; Page 27; 67pp; English.
XX
CC In order to change the VP2 Faragher sequence in pCEN120 to VP2 STC
CC sequence, five codons were changed in the VP2 ORF using PCR site
CC directed mutagenesis. Oligonucleotide primers RG677 plus RG678 and
CC RG685 plus RG686P were used to amplify a 530 bp and a 270 bp fragment
CC respectively from pCEN100. The gel purified 270 bp fragment was further
CC amplified using oligonucleotides RG702 and RG704. These purified
CC fragments which contain the five STC codon changes, were ligated into
CC pCEN120. The resulting plasmid, pVP2-STC was confirmed by DNA sequence
CC analysis. See also AAQ36873-906.
XX
SQ Sequence 39 BP; 10 A; 12 C; 10 G; 7 T; 0 other;

```
  Query Match             54.8%;  Score 12.6;  DB 14;  Length 39;
  Best Local Similarity   78.9%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      4 aacacccgctctctcgcaa 22
          |||||  |||||| | |||
Db      3 aacacgagctctcccccaa 21
```

Search completed: March 9, 2002, 01:07:00
Job time: 11946 sec